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Title of Thesis: Advanced studies on some Geminiviruses affecting
 kidney beans

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ABSTRACT

Symptomatic leaf samples were collected from bean fields cultivated in different governorates and tested by PCR using Geminivirus degenerate primers and *Squash Leaf Curl Virus* (SLCV) specific primers. All bean varieties grown in surveyed fields were found susceptible to Geminivirus infection and the dominant Geminivirus affecting bean plants was SLCV. Percentage of infection was higher at Nili season than that at the Summer season. *Squash leaf curl virus* (SLCV) was isolated from naturally infected common bean plants grown in Egypt and transmitted from naturally infected common bean onto twenty two species and varieties belonging to six different families *i.e.* *Moraceae*, *Solanaeae*, *Cucurbitaceae*, *Fabaceae*, *Chenopodiaceae*, and *Malvaceae* using viruliferous whitefly (*Bemisia tabaci*). Results revealed that SLCV could be transmitted to 16 out of 22 species tested and positively back inoculated to beans from these hosts. Six different commercial varieties of bean were evaluated for SLCV infection at three different growth stages. The evaluation was performed by whitefly inoculation in insect proof green house. Two commercial varieties (Tema and Giza 6) were found to be tolerant to SLCV infection in all tested growth stages. The disease severity of the viral infection varied in the other four susceptible varieties at the different growth stages. It was observed that infection percentage and disease severity were decreased with increasing growth stage. Significant difference in the percentage of yield loss in inoculated plants at age 15d and 25d from planting compared with control was recorded. On the other hand percentage of yield loss in plants inoculated at 35d stage was non-significant. The coat protein gene of SLCV was PCR amplified from infected common bean plants. SLCV-CP was cloned in pJET cloning vector and directly sequenced. The sequence alignment and phylogenetic analysis showed a relatively high diversity among the three different isolates that the identity ranged from 89 to 94%. Nucleotide sequencing of the complete genome of the virus was as follow, DNA-A (2667 bp) and DNA-B (2621 bp). The obtained sequences were submitted into the GenBank with accession numbers KJ624994 and ̧. The full nucleotide sequence of DNA-A, DNA-B and all open reading frames (ORF) of the SLCV-bean was aligned and compared with eleven different isolates of the SLCV available in the GenBank. The phylogenetic analysis of the complete nucleotide sequence revealed that SLCV is related to other isolates of SLCV from other governorates in Egypt (Cairo and Ismailia) as well as isolates from Lebanon (SLCV-LB2), Palestine (SLCV-Pal), Jordan (SLCV-JO) and Israel (SLCV-IL) sharing high identities ranging from (90% to 97%).

Key words: Common bean, virus incidence, *Squash Leaf Curl Virus*, PCR detection, cp sequence analysis, phylogenetic analysis, Egypt

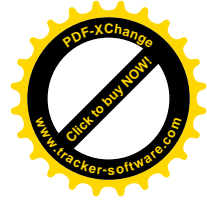
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المستخلص العربي

تم جمع عينات ورقية من حقول الفاصوليا المزروعة في عدة محافظات و كان يظهر عليها اعراض موزيك و التفاف اوراق و تجعد بجانب وجود تعداد كبير من الحشره الناقله (الذبابة البيضاء) ، وقد تم فحصها باستخدام تفاعل البلمره المتسلسل باستخدام بادئات متخصصه للكشف عن مجموعة الفيروسات التوأمية و كذلك استخدام بادئات متخصصه للكشف عن فيروس تجعد اوراق الكوسه ، وقد اظهرت نتائج الفحص ان غالبية النباتات المختبره كانت مصابه بالفيروسات التوأمية و ان اغلب الاصابات كانت بفيروس تجعد اوراق الكوسه. كما تم دراسة المدي العوائل لفيروس التفاف اوراق الكوسه بطريقة العدوي بالذبابه البيضاء علي 22 نوع نباتي تنتمي الي 6 عائلات مختلفه و اظهرت النتائج اصابة 16 نوع منها بالفيروس ، وكانت كل اصناف الفاصوليا المنزرعه في مصر قابله للاصابه. كما تم دراسة تأثير فيروس التفاف اوراق الكوسه علي ستة اصناف تجاريه من الفاصوليا بعمل عدوي باستخدام الذبابة البيضاء في ثلاث اعمار مختلفه من نمو النبات (15،25،35) يوم من الزراعه ، و اظهرت النتائج انه كلما زاد عمر النبات قلة نسبة الاصابه وكذلك شدة ظهور الاعراض و كذلك قلة نسبة الفقد في المحصول ، وكان اكثر الاصناف تحملا للاصابه في كافة الاعمار هما جيزه 6 و تيماء علي الترتيب.

كما تم عمل كلونه و تحليل للتابع النيكلوتيدي لجزء من جين الغطاء البروتيني في ثلاث عزلات من محافظات مختلفه و مقارنتها بالعزلات الموجود ببنك الجينات و تراوحت درجة القرابه من 89% الي 94%، مما يدل علي احتمالية وجود اكثر من عزله من الفيروس تصيب الفاصوليا.

كما تم عمل كلونه و تحليل للتابع النيكلوتيدي للجينوم الكامل لفيروس التفاف اوراق الكوسه و اظهرت النتائج ان الجينوم الفيروسي يتكون من 2 جزء ، الاول component A يحتوي علي خمس جينات و الثاني component B يحتوي علي اثنين من الجينات. و بالمقارنه بين العزله المصريه و العزلات الموجوده ببنك الجينات و جد ان درجة القرابه بين العزله المصريه و العزلات الاخرى تتراوح بين 90 و 97% . كما تم تسجيل هذه العزله ببنك الجينات تحت رقم KJ624994 بالنسبه component A و KJ579954 بالنسبه الي component B.



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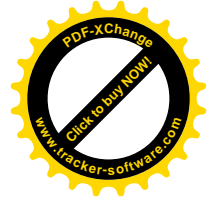
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